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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/898,586

DATE: 09/13/2001

TIME: 12:51:18

Input Set : A:\Cural381.app

Output Set: N:\CRF3\09132001\I898586.raw

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3 <110> APPLICANT: Gerlach, Valerie L
 4 MacDougall, John R
 5 Smithson, Glennnda
 7 <120> TITLE OF INVENTION: Novel Polypeptides and Nucleic Acids Encoding Same
 9 <130> FILE REFERENCE: 15966-638CIP
 11 <140> CURRENT APPLICATION NUMBER: 09/898,586
 C--> 12 <141> CURRENT FILING DATE: 2001-08-27
 14 <150> PRIOR APPLICATION NUMBER: 60/177,839
 15 <151> PRIOR FILING DATE: 2000-01-25
 17 <150> PRIOR APPLICATION NUMBER: 60/176,134
 18 <151> PRIOR FILING DATE: 2000-01-14
 20 <150> PRIOR APPLICATION NUMBER: 60/175,989
 21 <151> PRIOR FILING DATE: 2000-01-13
 23 <150> PRIOR APPLICATION NUMBER: 60/218,324
 24 <151> PRIOR FILING DATE: 2000-07-14
 26 <150> PRIOR APPLICATION NUMBER: 60/220,253
 27 <151> PRIOR FILING DATE: 2000-07-24
 29 <150> PRIOR APPLICATION NUMBER: 60/178,191
 30 <151> PRIOR FILING DATE: 2000-01-26
 32 <150> PRIOR APPLICATION NUMBER: 60/178,227
 33 <151> PRIOR FILING DATE: 2000-01-26
 35 <150> PRIOR APPLICATION NUMBER: 60/220,590
 36 <151> PRIOR FILING DATE: 2000-07-25
 38 <150> PRIOR APPLICATION NUMBER: 09/761,288
 39 <151> PRIOR FILING DATE: 2001-01-16
 41 <160> NUMBER OF SEQ ID NOS: 104
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 47 <212> TYPE: DNA
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 53 tctttgcact tttctgtgt ctctatttaa cagggtgtt tggaaactta ctcatcttgc 180
 54 tggccattgg ctcggtacac tgccttcaca caccatgta tttcttcctt gccaatctgt 240
 55 ccttggtaga cctctgcctt ccctcagcca cagtcccaa gatgctactg aacatccaaa 300
 56 cccaaaccca aaccatctcc tatcccggtt gcttggctca gatgtatttc tgtatgatgt 360
 57 ttgccaatat ggacaatttt cttctcacag tgatggcata tgaccgttac gtggccatct 420
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 60 acttctgctc tgataatgtt atccaccatt tcttctgtga tatcaactct ctctccctc 600
 61 tgtcctgttc cgacaccagt cttaacagt tgagtgttct ggctacgggt gggctgatct 660
 62 ttgtggtacc ttcagtgtgt atcctgggtat cctatatact cattgtttct gctgtgatga 720
 63 aagtcccttc tgcccaagga aaactcaagg ctttctctac ctgtggatct caccttgcct 780
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66 cattcatttta cagttttaaga aacaatgaac tgaagggggac tttaaaaaag accctaagcc 960
67 gaccggggcgc ggtgggtcac gcctgtaatc ccagcacttt gggaggccga ggcgggtgga 1020
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80 Phe Ser Ser Trp Gln Gln Gln Val Leu Leu Phe Ala Leu Phe Leu
81 20 25 30
83 Cys Leu Tyr Leu Thr Gly Leu Phe Gly Asn Leu Leu Ile Leu Leu Ala
84 35 40 45
86 Ile Gly Ser Asp His Cys Leu His Thr Pro Met Tyr Phe Phe Leu Ala
87 50 55 60
89 Asn Leu Ser Leu Val Asp Leu Cys Leu Pro Ser Ala Thr Val Pro Lys
90 65 70 75 80
92 Met Leu Leu Asn Ile Gln Thr Gln Thr Gln Thr Ile Ser Tyr Pro Gly
93 85 90 95
95 Cys Leu Ala Gln Met Tyr Phe Cys Met Met Phe Ala Asn Met Asp Asn
96 100 105 110
98 Phe Leu Leu Thr Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His
99 115 120 125
101 Pro Leu His Tyr Ser Thr Ile Met Ala Leu Arg Leu Cys Ala Ser Leu
102 130 135 140
104 Val Ala Ala Pro Trp Val Ile Ala Ile Leu Asn Pro Leu Leu His Thr
105 145 150 155 160
107 Leu Met Met Ala His Leu His Phe Cys Ser Asp Asn Val Ile His His
108 165 170 175
110 Phe Phe Cys Asp Ile Asn Ser Leu Leu Pro Leu Ser Cys Ser Asp Thr
111 180 185 190
113 Ser Leu Asn Gln Leu Ser Val Leu Ala Thr Val Gly Leu Ile Phe Val
114 195 200 205
116 Val Pro Ser Val Cys Ile Leu Val Ser Tyr Ile Leu Ile Val Ser Ala
117 210 215 220
119 Val Met Lys Val Pro Ser Ala Gln Gly Lys Leu Lys Ala Phe Ser Thr
120 225 230 235 240
122 Cys Gly Ser His Leu Ala Leu Val Ile Leu Phe Tyr Gly Ala Ile Thr
123 245 250 255
125 Gly Val Tyr Met Ser Pro Leu Ser Asn His Ser Thr Glu Lys Asp Ser
126 260 265 270
128 Ala Ala Ser Val Ile Phe Met Val Val Ala Pro Val Leu Asn Pro Phe
129 275 280 285
131 Ile Tyr Ser Leu Arg Asn Asn Glu Leu Lys Gly Thr Leu Lys Lys Thr
132 290 295 300
134 Leu Ser Arg Pro Gly Ala Val Ala His Ala Cys Asn Pro Ser Thr Leu
135 305 310 315 320
137 Gly Gly Arg Gly Gly Trp Ile Met Arg Ser Gly Asp Arg Asp His Pro

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147 <213> ORGANISM: Homo sapiens
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151 gatttcctct gtcataggga tatgggagac aatataacat ccatcagaga gttcctccta 120
152 ctgggatttc ccgttgcccc aaggattcag atgctcctct ttgggctctt ctccctgttc 180
153 tacgtcttca cctgctggg gaacgggacc atactggggc tcatctcact ggactccaga 240
154 ctgcacgccc ccatgtactt ctctctctca cacctggcgg tcgtcgacat cgcctacgcc 300
155 tgcaacacgg tgccccggat gctggtgaac ctctgcatc cagccaagcc catctccttt 360
156 gcgggcccga tgatgcagac ctttctgttt tccacttttg ctgtcacaga atgtctcttc 420
157 ctggtggtga tgtcctatga tctgtacgtg gccatctgcc accccctccg atatttggcc 480
158 atcatgacct ggagagtctg catcacctc gcggtgactt cctggaccac tggagtcttt 540
159 ttatccttga ttcatcttgt gttacttcta cctttaccct tctgtaggcc ccagaaaatt 600
160 tatcactttt tttgtgaaat cttggctgtt ctcaaacttg cctgtgcaga taccacatc 660
161 aatgagaaca tggctcttggc cggagcaatt tctgggctgg tgggaccctt gtccacaatt 720
162 gtagtttcat atatgtgcat cctctgtgct atccttcaga tccaatcaag ggaagttcag 780
163 aggaaagcct tccgcacctg cttctccccc ctctgtgtga ttggactcgt ttatggcaca 840
164 gccattatca tgtatgttgg acccagatat gggaacccca aggagcagaa gaaatatctc 900
165 ctgctgtttc acagcctctt taatcccatg ctcaatcccc ttatctgtag tcttaggaac 960
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180 20 25 30
182 Phe Tyr Val Phe Thr Leu Leu Gly Asn Gly Thr Ile Leu Gly Leu Ile
183 35 40 45
185 Ser Leu Asp Ser Arg Leu His Ala Pro Met Tyr Phe Phe Leu Ser His
186 50 55 60
188 Leu Ala Val Val Asp Ile Ala Tyr Ala Cys Asn Thr Val Pro Arg Met
189 65 70 75 80
191 Leu Val Asn Leu Leu His Pro Ala Lys Pro Ile Ser Phe Ala Gly Arg
192 85 90 95
194 Met Met Gln Thr Phe Leu Phe Ser Thr Phe Ala Val Thr Glu Cys Leu
195 100 105 110
197 Leu Leu Val Val Met Ser Tyr Asp Leu Tyr Val Ala Ile Cys His Pro
198 115 120 125
200 Leu Arg Tyr Leu Ala Ile Met Thr Trp Arg Val Cys Ile Thr Leu Ala
201 130 135 140
203 Val Thr Ser Trp Thr Thr Gly Val Leu Leu Ser Leu Ile His Leu Val

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204 145          150          155          160
206 Leu Leu Leu Pro Leu Pro Phe Cys Arg Pro Gln Lys Ile Tyr His Phe
207          165          170          175
209 Phe Cys Glu Ile Leu Ala Val Leu Lys Leu Ala Cys Ala Asp Thr His
210          180          185          190
212 Ile Asn Glu Asn Met Val Leu Ala Gly Ala Ile Ser Gly Leu Val Gly
213          195          200          205
215 Pro Leu Ser Thr Ile Val Val Ser Tyr Met Cys Ile Leu Cys Ala Ile
216          210          215          220
218 Leu Gln Ile Gln Ser Arg Glu Val Gln Arg Lys Ala Phe Arg Thr Cys
219 225          230          235          240
221 Phe Ser His Leu Cys Val Ile Gly Leu Val Tyr Gly Thr Ala Ile Ile
222          245          250          255
224 Met Tyr Val Gly Pro Arg Tyr Gly Asn Pro Lys Glu Gln Lys Lys Tyr
225          260          265          270
227 Leu Leu Leu Phe His Ser Leu Phe Asn Pro Met Leu Asn Pro Leu Ile
228          275          280          285
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231          290          295          300
233 Gly Val Glu Arg Ala Leu
234 305          310
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238 <211> LENGTH: 1090
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240 <213> ORGANISM: Homo sapiens
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244 tgggtttctc cagcctgggg gagctccagc tgctgctttt tgtcatcttt cttctcctat 120
245 acttgacaat cctgggtggcc aatgtgacca tcatggccgt tattcgcttc agctggactc 180
246 tccacactcc catgtatggc tttctattca tcttttcatt ttctgagtc tctacactt 240
247 ttgtcatcat ccctcagctg ctgggtccacc tgctctcaga caccaagacc atctccttca 300
248 tggcctgtgc caccagctg ttctttttcc ttggctttgc ttgcaccaac tgcctcctca 360
249 ttgctgtgat gggatatgat cgctatgtag caatttgtca ccctctgagg tacacactca 420
250 tcataaacia aaggctgggg ttggagtga tttctctctc aggagccaca ggtttcttta 480
251 ttgcttttgt ggccaccaac ctcatttgtg acatgcgttt ttgtggcccc aacagggtta 540
252 accactatct ctgtgacatg gcacctgtta tcaagttagc ctgcactgac acctatgtga 600
253 aagagctggc tttatttagc ctccagcatcc tggtaattat ggtgcctttt ctgttaattc 660
254 tcatactcta tggcttcata gttaacacca tctgaagat cccctcagct gagggaaga 720
255 aggcctttgt cacctgtgac tcacatctca ctgtggtctt tgtccactat ggctgtgcct 780
256 ctatcatcta tctgcggccc aagtccaagt ctgcctcaga caaggatcag ttggtggcag 840
257 tgacctacac agtggttact cccttactta atcctcttgt ctacagtctg aggaacaaag 900
258 aggtaaaaac tgcattgaaa agagttcttg gaatgcctgt ggcaaccaag atgagctaac 960
259 aaaaaataat aataaaatta actaggatag tcacagaaga aatcaaaggc ataaaatttt 1020
260 ctgaccttta atgcatgtct cagacagtgt ttccaaggat taagactact cttgcctttt 1080
261 tattttctcc                                     1090
264 <210> SEQ ID NO: 6
265 <211> LENGTH: 314
266 <212> TYPE: PRT
267 <213> ORGANISM: Homo sapiens

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Input Set : A:\Cura1381.app

Output Set: N:\CRF3\09132001\I898586.raw

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274 20 25 30
276 Leu Leu Leu Tyr Leu Thr Ile Leu Val Ala Asn Val Thr Ile Met Ala
277 35 40 45
279 Val Ile Arg Phe Ser Trp Thr Leu His Thr Pro Met Tyr Gly Phe Leu
280 50 55 60
282 Phe Ile Leu Ser Phe Ser Glu Ser Cys Tyr Thr Phe Val Ile Ile Pro
283 65 70 75 80
285 Gln Leu Leu Val His Leu Leu Ser Asp Thr Lys Thr Ile Ser Phe Met
286 85 90 95
288 Ala Cys Ala Thr Gln Leu Phe Phe Phe Leu Gly Phe Ala Cys Thr Asn
289 100 105 110
291 Cys Leu Leu Ile Ala Val Met Gly Tyr Asp Arg Tyr Val Ala Ile Cys
292 115 120 125
294 His Pro Leu Arg Tyr Thr Leu Ile Ile Asn Lys Arg Leu Gly Leu Glu
295 130 135 140
297 Leu Ile Ser Leu Ser Gly Ala Thr Gly Phe Phe Ile Ala Leu Val Ala
298 145 150 155 160
300 Thr Asn Leu Ile Cys Asp Met Arg Phe Cys Gly Pro Asn Arg Val Asn
301 165 170 175
303 His Tyr Phe Cys Asp Met Ala Pro Val Ile Lys Leu Ala Cys Thr Asp
304 180 185 190
306 Thr His Val Lys Glu Leu Ala Leu Phe Ser Leu Ser Ile Leu Val Ile
307 195 200 205
309 Met Val Pro Phe Leu Leu Ile Leu Ile Ser Tyr Gly Phe Ile Val Asn
310 210 215 220
312 Thr Ile Leu Lys Ile Pro Ser Ala Glu Gly Lys Lys Ala Phe Val Thr
313 225 230 235 240
315 Cys Ala Ser His Leu Thr Val Val Phe Val His Tyr Gly Cys Ala Ser
316 245 250 255
318 Ile Ile Tyr Leu Arg Pro Lys Ser Lys Ser Ala Ser Asp Lys Asp Gln
319 260 265 270
321 Leu Val Ala Val Thr Tyr Thr Val Val Thr Pro Leu Leu Asn Pro Leu
322 275 280 285
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325 290 295 300
327 Leu Gly Met Pro Val Ala Thr Lys Met Ser
328 305 310
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332 <211> LENGTH: 1090
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338 tgggtttctc cagcctgggg gagctccagc tgctactttt tgtcatcttt cttctcctat 120
339 acttgacaat cctggtggcc aatgtgacca tcatggcctg tattegttc agctggactc 180

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Use of n and / or Xaa has been detected in the Sequence Listing. Review the Sequence Listing to ensure a corresponding explanation is present in the <220> to <223> fields of each sequence using n or Xaa.

VERIFICATION SUMMARY

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Input Set : A:\Cura1381.app

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L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:679 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14

L:1642 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:35

L:1645 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:35

L:2209 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:49

L:2212 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:49

L:2749 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:63

L:2752 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:63